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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:20:45 ; Search time 5.40155 Seconds

(Without alignments)  
798.574 Million cell updates/sec

Title: US-09-622-613B-4

Perfect score: 579

Sequence: 1 ODMLTFQKKHLLTFRDVCN.....TFCVTCENQAPVHVGVCNC 104

Scoring table: BLOSUM62

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	547	94.5	104	1	RN30_RANPI
2	286	49.4	111	1	RNPO_RANCA
3	279.5	48.3	111	1	LECS_RANCA
4	263.5	45.5	111	1	RNPL_RANCA
5	142	24.5	119	1	RNP_IGUG
6	124.5	21.5	145	1	ANGR_MOUSE
7	124.5	21.5	146	1	ANGI_CERAE
8	123	21.2	124	1	RNP_GALMU
9	120	20.7	148	1	ANGI_BOVIN
10	118	20.4	128	1	RNP_MYOCO
11	117	20.2	138	1	RNP_CAVPO
12	116	20.0	124	1	RNP_BALAC
13	115.5	19.9	146	1	ANGI_MACMU
14	112.5	19.4	145	1	ANGI_MOUSE
15	112.5	19.4	146	1	ANGI_PAPHA
16	111	19.2	128	1	RNP_PROGU
17	110.5	19.1	155	1	ECPP_MOUSE
18	110	19.0	125	1	ANGI_RABIT
19	110	19.0	128	1	RNP_HYDXY
20	110	19.0	146	1	ANGI_MOTIA
21	108.5	18.7	147	1	RNLA_HUMAN
22	108	18.7	124	1	RNP_CHIBR
23	108	18.7	150	1	RNP_BOVIN
24	107	18.5	156	1	ECPP_MOUSE
25	106	18.3	147	1	ANGI_HUMAN
26	106	18.3	147	1	ANGI_PANTR
27	105	18.1	124	1	RNP_AEPME
28	105	18.1	124	1	RNP_AETAM
29	105	18.1	124	1	RNP_HIPAM
30	105	18.0	123	1	RNP_SHEEP
31	104.5	18.0	150	1	ANGI_PIG
32	104.5	18.0	150	1	RNK6_SAISC
33	104	18.0	124	1	RNP_BUBBU

34	104	18.0	124	1	RNP_CONTA	P00660 connochaete
35	104	18.0	124	1	RNP_GAZPH	P07848 gazella tho
36	103	17.8	123	1	ANG2_BOVIN	P80929 bos taurus
37	103	17.8	124	1	RNP_GIRCA	P00662 giraffa cam
38	103	17.8	124	1	RNP_PIG	P00671 sus scrofa
39	103	17.8	128	1	RNP_HYSCR	P04060 hystrix cri
40	103	17.8	156	1	RNP_MYOC	P39873 bos taurus
41	103	17.8	167	1	RNBR_BOVIN	P00674 equus cabal
42	102	17.6	128	1	RNP_HORSE	P00674 equus cabal
43	102	17.6	146	1	ANGI_SAGOE	P07426 mus musc
44	101.5	17.5	155	1	ECPI_MOUSE	P07426 mus musc
45	101	17.4	141	1	RNBR_GIRCA	P00662 giraffa cam

## ALIGNMENTS

RESULT 1	ID	Sequence	Standard	PRT	104 AA
AC	P22069	01-AUG-1991 (Rel. 19, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DE	01-FEB-1995 (Rel. 31, Last annotation update)				
OS	P-30 protein (EC 3.1.27.-) (onconase).				
OC	Rana pipiens (Northern leopard frog).				
OC	Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:				
OC	Amphibia: Batrachia: Anura: Neobatrachia: Ranioidea: Rana.				
OX	NCBI TaxID=8404;				
RN	[1]				
RC	SEQUENCE.				
RC	TISSUE=Embryo;				
RX	MEDLINE=91093131; PubMed=1985896;				
RA	Ardelet W., Mikulski S.M., Shogen K.;				
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";				
RL	J. Biol. Chem. 266:245-251(1991).				
RN	[2]				
RP	3D-STRUCTURE MODELING.				
RX	MEDLINE=93066156; PubMed=1438177;				
RA	Mosimann S.C., Johns K.L., Ardelet W., Mikulski S.M., Shogen K.;				
RT	James M.N.G.;				
RT	"Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens oocytes and early embryos.";				
RL	Proteins. 14:392-400(1992).				
RN	[3]				
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).				
RX	MEDLINE=94166079; PubMed=8120892;				
RA	Mosimann S.C., Ardelet W., James M.N.G.;				
RT	"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";				
RL	J. Mol. Biol. 236:1141-1153(1994).				
CC	-I- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH MOLECULAR WEIGHT RIBOSOMAL RNA.				
CC	-I- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).				
CC	-I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.				
DR	PDB: 1ONC; 31-JAN-94.				
DR	InterPro: IPR001427; RnaseA.				
DR	Pfam: PF00074; RnaseA. 1.				
DR	PRODOM: PD000535; RnaseA. 1.				
DR	SMART: SM00092; Rnase_Pc. 1.				
DR	PROSITE: PS00127; Rnase_PANCREATIC. 1.				
KW	Hydroxylase; Nuclease; Endonuclease; 3d-structure.				
FT	MOD_RES				
FT	ACT_SITE				
FT	ACT_SITE				
FT	ACT_SITE				
FT	ACT_SITE				
FT	DISULFID				
FT	DISULFID				
FT	DISULFID				
FT	DISULFID				

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FT DISULFID 87 104
RT HELIX 3 10
FT STRAND 11 12
FT HELIX 19 22
FT TURN 23 24
FT TURN 26 30
FT STRAND 33 38
FT HELIX 41 48
FT TURN 49 50
FT STRAND 55 58
FT STRAND 63 70
FT TURN 74 75
FT STRAND 77 84
FT STRAND 86 91
FT TURN 92 93
FT STRAND 94 101
SQ SEQUENCE 104 AA: 11845 MW: 22A753C2P9E566B4 CRC64:

Query Match 94.5%; Score 547; DB 1; Length 104;
Best Local Similarity 94.2%; Pred. No. 1.7e-51;
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFTYSRPEPYKAICGIIASKNVLT 60
DB 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFTYSRPEPYKAICGIIASKNVLT 60
QY 61 FEFYLSDCNVTSRPCCKKLKSTNTFCVTGENAPVHFVGVC 104
DB 61 SEFLSDCNVTSRCKKTKLKSTNKFVTCENQAPVHFVGVC 104

RESULT 2
RNPO_RANCA STANDARD; PRT; 111 AA.
ID RNPO_RANCA
AC P11916:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Stallic acid-binding
DE lectin) (SBL-C).
OS Rana catesbeiana (bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP TISSUE-Egg;
RC MEDLINE=67299649; PubMed=3304421.
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
RA Takayanagi G., Hakomori S.;
RT "Amino acid sequence of stallic acid binding lectin from frog (Rana
RT catesbeiana) eggs.";
RL Biochemistry 26:2189-2194(1987).
RN [2]
RP CHARACTERIZATION, AND SEQUENCE OF 59-79.
RX MEDLINE=92220613; PubMed=1373237.
RA Liao Y.-D.;
RT "A pyrimidine-quanine sequence-specific ribonuclease from Rana
RT catesbeiana (bullfrog) oocytes.";
RL Nucleic Acids Res. 20:1371-1377(1992).
RN [3]
RP CHARACTERIZATION.
RC TISSUE-Egg;
RX MEDLINE=93192604; PubMed=8448385.
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
RA Takayanagi Y., Hakomori S., Titani K.;
RT "Ribonuclease activity of stallic acid-binding lectin from Rana
RT catesbeiana eggs.";
RL Glycobiology 3:37-45(1993).
RN [4]
RP STRUCTURE BY NMR.
RX MEDLINE=98437383; PubMed=9761686;
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;

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RT "The solution structure of a cytotoxic ribonuclease from the oocytes
RT of Rana catesbeiana (bullfrog).";
RL J. Mol. Biol. 283:231-244(1998).
CC -1- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE
CC RESIDUES WITH A 3' FLANKING GUANINE. HYDOLYSES POLY(U) AND POLY(C)
CC AS SUBSTRATES, AND PREFERS THE FORMER. THE S-LECTINS IN FROG EGGS
CC MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG
CC EMBRYO. THIS LECTIN AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING
CC NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND
CC HUMAN ORIGIN.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: A27121; A27121.
DR PDB: 1BC4; 28-OCT-98.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolyase; Nuclease; Endonuclease; Stallic acid; lectin; 3D-structure.
FT ACT_SITE 10 10
FT ACT_SITE 35 35
FT ACT_SITE 103 103
FT DISULFID 19 71
FT DISULFID 34 81
FT DISULFID 52 96
FT DISULFID 93 110
SQ SEQUENCE 111 AA: 12464 MW: 0BC9E5F5729ECP4 CRC64:

Query Match 49.4%; Score 286; DB 1; Length 111;
Best Local Similarity 48.6%; Pred. No. 9.5e-24;
Matches 54; Conservative 16; Mismatches 33; Indels 8; Gaps 3;

QY 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFTYSRPEPYKAICGIIASKNV 56
DB 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFTYSRPEPYKAICGIIASKNV 56
QY 57 VLTFFEFLSDC---NWTSRPCCKKLKSTNTFCVTGENAPVHFVGVC 104
DB 60 VLSSTRQLNVTGRTSITPRCPYSSRTETNYICVGENQPVHFGAGIGRC 110

RESULT 3
LECS_RANJA STANDARD; PRT; 111 AA.
ID LECS_RANJA
AC P18839;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stallic acid-binding lectin (EC 3.1.27.-).
OS Rana japonica (Japanese reddish frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE-Egg;
RX MEDLINE=91035319; PubMed=2229005;
RA Kaniya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
RA Takayanagi Y., Titani K.;
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT eggs.";
RL Biochem. 108:139-143(1990).
CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
CC PREFERENTIALLY AGGLUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT
CC DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: JX0120; JX0120.

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DR HSSP; P11916; 1BC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA: 1.
DR ProDom: PD000535; RNaseA: 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; Lectin.
FT ACT_SITE 10 10 PYROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 35 35 BY SIMILARITY.
FT ACT_SITE 103 103 BY SIMILARITY.
FT ACT_SITE 103 103 BY SIMILARITY.
FT DISULFID 19 72
FT DISULFID 34 82
FT DISULFID 52 97
FT DISULFID 94 111
SQ SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

Query Match 48.3%; Score 279.5; DB 1; Length 111;
Best Local Similarity 44.1%; Pred. No. 4,7e-23;
Matches 49; Conservative 19; Mismatches 36; Indels 7; Gaps 2;

QY 1 QDMVTFQKHLTNRDVDCNNILSTNLF---HCKDKNTFIYSRPEPVKATCKGIASKN 56
ID 1 QNNAKFEKHIRPNTSNTNCNTIMDKSIYIVGGCKERNTFISSATTYKAIKSGASTNRN 60
Db 1 QNNAKFEKHIRPNTSNTNCNTIMDKSIYIVGGCKERNTFISSATTYKAIKSGASTNRN 60

QY 57 VLTTFEFLSDC---NNTSRPCKYKLLKSTNTEFCVTCENQAPVHFGVGHG 104
ID 57 VLTTFEFLSDC---NNTSRPCKYKLLKSTNTEFCVTCENQAPVHFGVGHG 104
Db 61 VLTTFEFLSDC---NNTSRPCKYKLLKSTNTEFCVTCENQAPVHFGVGHG 111

RESULT 4
RNP_LIGUIC STANDARD; PRT; 111 AA.
AC P14626;
DT 01-FEB-1990 (Rel. 14, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease, liver (EC 3.1.27.5).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=90130374; Pubmed=2613682;
RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
  Okazaki T., Ohgi K., Irie M.;
RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
  liver.";
FT MOD_RES 1 PYROLIDONE CARBOXYLIC ACID.
FT DISULFID 25 80 BY SIMILARITY.
FT DISULFID 39 91 BY SIMILARITY.
FT DISULFID 57 106 BY SIMILARITY.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 40 40 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.
SQ SEQUENCE 119 AA; 13324 MW; 6072FB5B7B15BD5A CRC64;

Query Match 24.5%; Score 142; DB 1; Length 119;
Best Local Similarity 29.8%; Pred. No. 2e-08;
Matches 34; Conservative 19; Mismatches 45; Indels 16; Gaps 5;

QY 1 QDMVTFQKHL-----TNTRDVCNNILSTNLFCKDKNFYSRPEPVKATCKGIASKN 49
ID 1 QNNAKFEKHIRPNTSNTNCNTIMDKSIYIVGGCKERNTFISSATTYKAIKSGASTNRN 60
Db 1 QNNAKFEKHIRPNTSNTNCNTIMDKSIYIVGGCKERNTFISSATTYKAIKSGASTNRN 60

QY 50 GIATSKVLTTFE-FYLSDC---NNTSRPCKYKLLKSTNTEFCVTCENQAPVHFGVGHG 98
ID 61 GTHEDNLYDSNESFDLTDCKNNGVGTAPSSCKYNGTGTCKRIIRIACENMGVHFG 114
Db 61 GTHEDNLYDSNESFDLTDCKNNGVGTAPSSCKYNGTGTCKRIIRIACENMGVHFG 114

RESULT 6
ANGR_MOUSE STANDARD; PRT; 145 AA.
ID ANGR_MOUSE

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Query Match 45.5%; Score 263.5; DB 1; Length 111;
Best Local Similarity 42.3%; Pred. No. 2.3e-21;
Matches 47; Conservative 19; Mismatches 38; Indels 7; Gaps 2;

QY 1 QDMVTFQKHLTNRDVDCNNILSTNLF---HCKDKNTFIYSRPEPVKATCKGIASKN 56
ID 1 QNNAKFEKHIRPNTSNTNCNTIMDKSIYIVGGCKERNTFISSATTYKAIKSGASTNRN 60
Db 1 QNNAKFEKHIRPNTSNTNCNTIMDKSIYIVGGCKERNTFISSATTYKAIKSGASTNRN 60

QY 57 VLTTFEFLSDC---NNTSRPCKYKLLKSTNTEFCVTCENQAPVHFGVGHG 104
ID 57 VLTTFEFLSDC---NNTSRPCKYKLLKSTNTEFCVTCENQAPVHFGVGHG 104
Db 61 VLTTFEFLSDC---NNTSRPCKYKLLKSTNTEFCVTCENQAPVHFGVGHG 111

RESULT 5
RNP_LIGUIC STANDARD; PRT; 119 AA.
AC P14626;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase A).
OS Iguana iguana (Common Iguana).
OC Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX NCBI_TaxID=8517;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=94139745; Pubmed=8307028;
RA Zhao W., Beintema J.J., Hofsteenge J.;
RT "The amino acid sequence of iguana (Iguana iguana) pancreatic
  ribonuclease.";
FT MOD_RES 1 PYROLIDONE CARBOXYLIC ACID.
FT DISULFID 25 80 BY SIMILARITY.
FT DISULFID 39 91 BY SIMILARITY.
FT DISULFID 57 106 BY SIMILARITY.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 40 40 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.
SQ SEQUENCE 119 AA; 13324 MW; 6072FB5B7B15BD5A CRC64;

Query Match 24.5%; Score 142; DB 1; Length 119;
Best Local Similarity 29.8%; Pred. No. 2e-08;
Matches 34; Conservative 19; Mismatches 45; Indels 16; Gaps 5;

QY 1 QDMVTFQKHL-----TNTRDVCNNILSTNLFCKDKNFYSRPEPVKATCKGIASKN 49
ID 1 QNNAKFEKHIRPNTSNTNCNTIMDKSIYIVGGCKERNTFISSATTYKAIKSGASTNRN 60
Db 1 QNNAKFEKHIRPNTSNTNCNTIMDKSIYIVGGCKERNTFISSATTYKAIKSGASTNRN 60

QY 50 GIATSKVLTTFE-FYLSDC---NNTSRPCKYKLLKSTNTEFCVTCENQAPVHFGVGHG 98
ID 61 GTHEDNLYDSNESFDLTDCKNNGVGTAPSSCKYNGTGTCKRIIRIACENMGVHFG 114
Db 61 GTHEDNLYDSNESFDLTDCKNNGVGTAPSSCKYNGTGTCKRIIRIACENMGVHFG 114

RESULT 6
ANGR_MOUSE STANDARD; PRT; 145 AA.
ID ANGR_MOUSE

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AC Q64438;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Angiogenin-related protein precursor.
GN ANGRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1].
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Liver;
RA MEDLINE=96079109; PubMed=8530072;
RA Brown W.E., Noble V., Subramanian V., Shapiro R.;
RT "The mouse angiogenin gene family: structures of an angiogenin-related
RT protein gene and two pseudogenes.";
RL Genomics 29:200-206(1995).
CC -1 SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U22519; AAA91367.1;
DR HSSP: P03950; 1A4Y.
DR MGD: MGI:104984; AngRP.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL; Hydrolase; Nuclease; Endonuclease.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT DISULFID 50 104
FT DISULFID 63 115
FT DISULFID 81 130
SQ SEQUENCE 145 AA; 16612 MW; 29A6EB814429C4AD CRC64;
Query Match 21.5%; Score 124.5; DB 1; Length 145;
Best Local Similarity 36.8%; Pred. No. 1.8e-06;
Matches 28; Conservative 11; Mismatches 30; Indels 7; Gaps 3;
OY 30 CKDKNTFIYSRPEVKAIC--KGIASKNV-LTTFEFLSDCNTSR---PCKYKLKKS 82
DB 63 CKDVTFTIHDTRKNKIKACGKSGSPYGRNLRISRSRCQVTTCTHKGSRPRPCRYRASKG 122
OY 83 TNFCVCNENQAPVHF 98
DB 123 FRYITICENGMPVHF 138
RESULT 7
ANGI_CERA_E STANDARD: PRT; 146 AA.
AC Q8WN66;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (Rnase 5).
GN ANG OR RNASE5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1].
RP SEQUENCE FROM N.A.
RC MEDLINE=21918422; PubMed=11919285;
RA Zhang J., Rosenberg H.F.;
RT "Diversifying selection of the tumor-growth promoter angiogenin in
RT primate evolution.";
RL Mol. Biol. Evol. 19:438-445(2002).
CC -1 FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
CC ANGIOGENIN IS ENDOCYTOTIC AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAS (By similarity).
CC -1 SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC -----
DR EMBL: AF41664; AAL61646.1;
DR HydroLase; Nuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal.
FT SIGNAL 1 24
FT CHAIN 25 146
FT MOD_RES 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 138 138
FT DISULFID 50 105
FT DISULFID 63 116
FT DISULFID 81 131
SQ SEQUENCE 146 AA; 16444 MW; 27860112E85B8DF9 CRC64;
Query Match 21.5%; Score 124.5; DB 1; Length 146;
Best Local Similarity 29.7%; Pred. No. 1.8e-06;
Matches 30; Conservative 17; Mismatches 31; Indels 23; Gaps 4;
OY 5 TFOKKHLTNPFDVDCNNILSTNLFCKDKNTFIYSRPEVKAIC--KGIASKNV-LTT 60
DB 53 TMRRRHLTSP-----CKDINFINGNNHHIKIGDSDNGNNGYENLRISK 97
OY 61 FEFLSDCNTVS---RPCKYKLKKSNTFCVCNENQAPVH 97
DB 98 SPFQVTTCTNLGSGSPRPPCQYRATRGSRNIVGCEGLPVH 138
RESULT 8
RNP_GALMU STANDARD: PRT; 124 AA.
AC P00680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).
GN RNASE1 OR RNS1.
OS Galea musteloides (Culs).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Canidae; Galea.
OX NCBI_TaxID=10146;
RN [1].
RP SEQUENCE.
RA MEDLINE=87036770; PubMed=6571219;
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RA Beintema J.J., Neuteboom B.;
RT "Origin of the duplicated ribonuclease gene in guinea-pig: comparison
RT of the amino acid sequences with those of two close relatives:
RT capybara and cuss ribonuclease."
RL J. Mol. Evol. 19:145-152(1983).
CC -I- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: PANCREAS.
CC -I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: A00827; NR01.
DR HSSP: P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA_1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT VARIANT 1 1 MISSING (IN 1/3 OF THE MOLECULES).
SQ SEQUENCE 124 AA; 13870 MW; 609C7E251A7BBA25 CRC64;

Query Match 21.2%; Score 123; DB 1; Length 124;
Best Local Similarity 28.2%; Pred. No. 2.2e-06;
Matches 33; Conservative 21; Mismatches 39; Indels 24; Gaps 7;

OY 4 LTPQKHL-----TNRDVCNNIL--STNLFHCKDKFTIYSRPEPKAIC--KGI 51
DB 6 MKFQRQHDSDGHPDPTN--YCNEMVVRSMTOGRCPVTFVHEPLEAVQAVCSQKRV 63
OY 52 IASKNVLTTFEY----LSDCNVTSRP----CKYLRKSTMTDFVCYTCEN--QAPVHF 98
DB 64 PCRKGQTCYOSHSMRTIDCRVTSSSKYPCNCTMTQAKNSIIVACGTSVPVHF 120

RESULT 9
ANGI_BOVIN STANDARD: PRT: 148 AA.
ID ANGI_BOVIN STANDARD: PRT: 148 AA.
AC P10152; O9GKP9;
DT 01-MAR-1989 (Rel. 10, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiogenin-1 precursor (EC 3.1.27.-).
GN ANGI OR ANG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Chang S.-I.;
RT "Cloning, sequencing, and expression of bovine angiogenin.";
RL submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 24-148.
RC TISSUE=Milk;
RX MEDLINE=89065101; PubMed=3197838;
RA Maes P., Damerit D., Rommens C., Montreuil J., Spik G., Tartar A.;
RT "The complete amino acid sequence of bovine milk angiogenin.";
RN FEBS Lett. 241:41-45(1988).
RP SEQUENCE OF 24-148.
RC TISSUE=Plasma;

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RX MEDLINE=89375344; PubMed=2775757;
RA Bond M.D., Struydom D.J.;
RT "Amino acid sequence of bovine angiogenin.";
RL Biochemistry 28:6110-6113(1989).
RN [4]
RP CHARACTERIZATION AND SEQUENCE OF 25-55.
RC TISSUE=Plasma;
RX MEDLINE=89118214; PubMed=3064806;
RA Bond M.D., Vallee B.L.;
RT "Isolation of bovine angiogenin using a placental ribonuclease
RT inhibitor binding assay.";
RL Biochemistry 27:6282-6287(1988).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=95224057; PubMed=7708754;
RA Acharya K.R., Shapiro R., Riordan J.F., Vallee B.L.;
RT "Crystal structure of bovine angiogenin at 1.5-A resolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).
RN [6]
RP STRUCTURE BY NMR.
RX MEDLINE=96280645; PubMed=8688423;
RA Leguin O., Albaret C., Bontems F., Spik G., Lallemand J.-Y.;
RT "Solution structure of bovine angiogenin by 1H nuclear magnetic
RT resonance spectroscopy.";
RL Biochemistry 35:8870-8880(1996).
CC -I- FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
CC ANGIOGENIN IS ENDOCTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAS. BINDS TIGHTLY TO PLACENTAL
CC RIBONUCLEASE INHIBITOR AND HAS VERY LOW RIBONUCLEASE ACTIVITY.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: SERUM, AND MILK.
CC -I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC -----
DR EMBL: AF135124; AAC47631.1;
DR PIR: A32474; A32474.
DR PDB: IAGI; 03-APR-96.
DR PDB: 1G10; 07-DEC-96.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA_1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal; 3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 148 ANGIOGENIN-1.
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 138 138
FT DISULFID 50 105
FT DISULFID 63 116
FT DISULFID 81 131
SQ SEQUENCE 148 AA; B7999124CB8523DD CRC64;

Query Match 20.7%; Score 120; DB 1; Length 148;
Best Local Similarity 32.7%; Pred. No. 5.6e-06;
Matches 32; Conservative 14; Mismatches 32; Indels 20; Gaps 5;

OY 16 DVDCCNNILSTNLF--HCKDKFTIYSRPEPKAIC-----GIASKNVLTTFEY 64

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Db          47 DEYCFNMKMRRLTRPCKDRNTFTHGNKNKDIKICEDNRNGOPYRGLRISKS-----EFQ 101
Oy          65 LSDC---NVTSR-PCKYKLRKSTNFCVTCENOAPVHF 98
           102 ITICKHKGSSRPPCRGATEDSRIVYGCENGLPVHF 139

RESULT 10
RNPB_CAVPO
ID RNPB_CAVPO STANDARD: PRT: 128 AA.
AC P00679;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic B (EC 3.1.27.5) (Rnase IB).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
NCBI_Taxid=10141;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=77185023; Pubmed=862624;
RA van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gaastra W.,
RA Beintema J.J.;
RT "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary
RT structure and glycosylation."
RL Eur. J. Biochem. 75:91-100(1977).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: A00826; NRGPB.
DR HSSP: P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA.1.
DR SMART: SM00092; RNase_Pc.1.
DR PROSITE: PS00127; RNASE_PANCREATIC.1.
KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84
FT DISULFID 40 95
FT DISULFID 58 110
FT DISULFID 65 72
FT ACT_SITE 12 12
FT ACT_SITE 41 41
FT ACT_SITE 119 119
FT CARBOHYD 21 21
FT CARBOHYD 34 34
FT VARIANT 64 64
SQ SEQUENCE 128 AA; 14406 MW; A2FA4101A1A33E93B CRC64;

Query Match 20.4%; Score 118; DB 1; Length 128;
Best Local Similarity 25.9%; Pred. No. 7.8e-06;
Matches 30; Conservative 25; Mismatches 39; Indels 22; Gaps 7;

Oy          4 LTFQKHL-----INTRDVDCNNTL---STNLFHCKDKNFTIYSRPEYKAIK---KGII 52
           6 MKFOGHNDPESPSNSSNY-CNVMMIRNMTOGCKRPVNTFVHSLADYQAVCFQKNVL 64
Oy          53 ASKNVLTFFERY---LSDCNVTSRP---CKYKLRKSTNFCVTCENO--APVHF 98
           65 CKNGQTCYOYSRMRITDCRVTSSSKFPNCSYRMSQAKSIIVACGEDPVPVPHF 120

RESULT 11
RNP_MYOCO
ID RNP_MYOCO STANDARD: PRT: 128 AA.
AC P00676;
DT 21-JUL-1986 (Rel. 01, Created)

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DT          21-JUL-1986 (Rel. 01, Last sequence update)
DT          15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase A).
GN RNASEI OR RNSI.
OS Myocastor coypus (Coypu) (Nutria).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Myocastoridae;
OC Myocastor.
NCBI_Taxid=10157;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=77065676; Pubmed=999896;
RA van den Berg A., van den Hende-Timmer L., Beintema J.J.;
RT "Isolation, properties and primary structure of coypu and chinchilla
RT pancreatic ribonuclease."
RL Biochim. Biophys. Acta 453:400-409(1976).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: A00822; NRCU.
DR HSSP: P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA.1.
DR SMART: SM00092; RNase_Pc.1.
DR PROSITE: PS00127; RNASE_PANCREATIC.1.
KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84
FT DISULFID 40 95
FT DISULFID 58 110
FT DISULFID 65 72
FT ACT_SITE 12 12
FT ACT_SITE 41 41
FT ACT_SITE 119 119
FT CARBOHYD 34 34
SQ SEQUENCE 128 AA; 14267 MW; 4EB924E52B445832 CRC64;

Query Match 20.2%; Score 117; DB 1; Length 128;
Best Local Similarity 28.2%; Pred. No. 1e-05;
Matches 33; Conservative 19; Mismatches 37; Indels 28; Gaps 7;

Oy          6 FQKHL-----INTRDVDCNNTL---STNLF-HCKDKNFTIYSRPEYKAIKGIASKNV 57
           8 FERQHNDSGSPSTPNPCNEMKSRMTOGCKRPVNTFVHSLADYQAVC---FQKNV 63
Oy          58 L-----TTFEFLSDCNVTSRP---CKYKLRKSTNFCVTCENO--APVHF 98
           64 CKNGQTCYOYSNMHITDCRVTSNSDYPNCSYRISOEKSIIIVACGNGPVPVPHF 120

RESULT 12
RNP_BALAC
ID RNP_BALAC STANDARD: PRT: 124 AA.
AC P00673;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase I) (Rnase A).
GN RNASEI OR RNSI.
OS Balaeoptera acutorostrata (Mink whale) (lesser rorqual).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaeopteridae; Balaeoptera.
NCBI_Taxid=9767;
RN [1]
RP SEQUENCE.
RX MEDLINE=76277855; Pubmed=962870;
RA Emmens M., Wellings G.W., Beintema J.J.;

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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AF41667; AAL61649.1;
CC
CC Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
CC Protein synthesis inhibitor; Signal.
CC SIGNAL 1 24
CC CHAIN 25 146
CC MOD_RES 25 25
CC
CC ACT_SITE 37 37
CC ACT_SITE 64 64
CC ACT_SITE 138 138
CC DISULFD 50 105
CC DISULFD 63 116
CC DISULFD 81 131
CC
CC SEQUENCE 146 AA; E39A89215DB2A2244 CRC64;
CC
CC Query Match 19.9%; Score 115.5; DB 1; Length 146;
CC Best Local Similarity 27.7%; Pred. No. 1.7e+05;
CC Matches 28; Conservative 17; Mismatches 33; Indels 23; Gaps 4;
CC
CC OY 5 TFQKKHLNTNTVDYDCNNILSTNLPHCKDKNTFTYSRPEYKAIC---KGIIASKNV-LTT 60
CC Db 53 TMRRRHLTSP-----CKDINFVHGNNRHIIAYALOGDEGSPYGCGNLRIST 97
CC
CC OY 61 FEFYLDSCNVTS---RPCKYKLEKSTPTFCVGENNAPV 97
CC Db 98 SPFOYTTCKLKGSPRPCCGYRATRGSRNIVYGCENGLPVH 138
CC
CC RESULT 14
CC ANGI_MOUSE STANDARD: PRT; 145 AA.
CC ID ANGI_MOUSE
CC AC P21570:
CC DT 01-MAY-1991 (Rel. 18, Created)
CC DT 01-MAY-1991 (Rel. 18, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Angiogenln precursor (EC 3.1.27.-).
CC GN ANG.
CC OS Mus musculus (Mouse).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC OX NCBI_TaxID=10090;
CC RN 11
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=91025023; PubMed=222458;
CC RA Bond M.D., Vallee B.L.;
CC RT "Isolation and sequencing of mouse angiogenln DNA.";
CC RL Biochem. Biophys. Res. Commun. 171:968-993(1990).
CC RN 12
CC RP PARTIAL SEQUENCE.
CC RC TISSUE=Serum;
CC RX MEDLINE=93192291; PubMed=8448182;
CC RA Bond M.D., Strydom D.J., Vallee B.L.;
CC RT "Characterization and sequencing of rabbit, pig and mouse
CC RT angiogenlns: discernment of functionally important residues and
CC RT regions.";
CC RL Biochim. Biophys. Acta 1162:177-186(1993).
CC
CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS: ONCE BOUND,
CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAs.
CC
CC -1- SUBCELLULAR LOCATION: Secreted.
CC
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY

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DR EMBL: U22516; AAA91366.1; -  
DR PIR: A35932; A35932.  
DR HSSP: P03950; 1A4Y.  
DR MGD: MGI:88022; Ang.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; RNaseA; 1.  
DR PRINTS: PR00794; RIBONUCLEASE.  
DR PRODOM: PD000535; RNaseA; 1.  
DR SMART: SM00092; RNase\_Pc; 1.  
DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
FT protein synthesis inhibitor; signal.  
FT SIGNAL 1 24  
FT CHAIN 25 145  
FT MOD\_RES 25 25  
FT ACT\_SITE 37 37  
FT ACT\_SITE 64 64  
FT ACT\_SITE 137 137  
FT DISULFID 50 104  
FT DISULFID 63 115  
FT DISULFID 81 130  
SQ SEQUENCE 145 AA; 16228 MW; 06944260DB764938 CRC64;  
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Query Match 19.4%; Score 112.5; DB 1; Length 145;  
Best Local Similarity 34.2%; Pred. No. 3.4e-05;  
Matches 26; Conservative 11; Mismatches 32; Indels 7; Gaps 3;  
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OY 30 CKDKNFTIYSRPEPKAIC--KGIASKNV-LITFEFYSDCNVTS---RPCKYKLUKS 82  
DB 63 CKDVTFTIHGKSKAIKICGANGSPYRENLMKSPQVYTKTKTGSPRCQYRMSAG 122  
OY 83 TITFCVTCENQAPVHF 98  
DB 123 FRHVIVACENGLPVHF 138  
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RESULT 15  
ANGI\_PAPHA  
ID ANGI\_PAPHA STANDARD: PRT: 146 AA.  
AC Q8WNE4;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).  
GN ANG OR RNASE5.  
OS Papio hamadryas (Hamadryas baboon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Papio.  
OX NCBI\_TaxID=9557;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21918422; PubMed=11919285;  
RA Zhang J., Rosenberg H.F.;  
RT "Diversifying selection of the tumor-growth promoter angiogenin in  
RT primate evolution".  
RL Mol. Biol. Evol. 19:438-445(2002).  
CC -!- FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS  
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,  
CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY  
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL  
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND  
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY

-----  
CC HYDROLYZING CELLULAR TRNAS (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
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DR EMBL: AF441666; AAL61648.1; -  
DR PIR: A441666; AAL61648.1; -  
DR HSSP: A441666; AAL61648.1; -  
DR MGD: MGI:16432; Ang.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; RNaseA; 1.  
DR PRINTS: PR00794; RIBONUCLEASE.  
DR PRODOM: PD000535; RNaseA; 1.  
DR SMART: SM00092; RNase\_Pc; 1.  
DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
FT protein synthesis inhibitor; signal.  
FT SIGNAL 1 24  
FT CHAIN 25 146  
FT MOD\_RES 25 25  
FT ACT\_SITE 37 37  
FT ACT\_SITE 64 64  
FT ACT\_SITE 138 138  
FT DISULFID 50 105  
FT DISULFID 63 116  
FT DISULFID 81 131  
SQ SEQUENCE 146 AA; 16432 MW; A4C3CED1482370FE CRC64;  
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Query Match 19.4%; Score 112.5; DB 1; Length 146;  
Best Local Similarity 27.7%; Pred. No. 3.5e-05;  
Matches 28; Conservative 16; Mismatches 34; Indels 23; Gaps 4;  
-----  
OY 5 TFOKHLITNRDVCNNILSTNLFHCCKDKNFTIYSRPEPKAIC--KGIASKNV-LTT 60  
DB 53 TMRRLHITSP-----CKDTFTIHGKSKAIKICGANGSPYRENLMKSPQVYTKTKTGSPRCQYRMSAG 97  
OY 61 FEYFLSDCNV---TSRCKYKLUKSKNTFCVTCENQAPVH 97  
DB 98 SPFOVYTKLHGSPRRCYRATRGSRNIVGCEGLPVH 138  
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Search completed: June 25, 2003, 14:50:02  
Job time : 5.40155 secs